

SEQUENCE LISTING

<110> KROPSHOFER, H.
VOGT, A.
ROEHN, T.A.

<120> Identification of novel MHC class II associated candidate tumor
antigens

<130> Case 21412

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<150> EP 02022224.6
<151> 2002-02-10

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<170> PatentIn version 3.2

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35 40 45

Gln Pro Ser Leu Leu Cys Val Arg Gly Thr Ser Ala Asp His Cys Val
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Gln Leu Ile Ala Ala Gln Glu Ala Asp Ala Ile Thr Leu Asp Gly Gly
65 70 75 80

Ala Ile Tyr Glu Ala Gly Lys Glu His Gly Leu Lys Pro Val Val Gly
85 90 95

Glu Val Tyr Asp Gln Glu Val Gly Thr Ser Tyr Tyr Ala Val Ala Val
100 105 110

Val Arg Arg Ser Ser His Val Thr Ile Asp Thr Leu Lys Gly Val Lys
115 120 125

Ser Cys His Thr Gly Ile Asn Arg Thr Val Gly Trp Asn Val Pro Val
130 135 140

Gly Tyr Leu Val Glu Ser Gly Arg Leu Ser Val Met Gly Cys Asp Val
145 150 155 160

Leu Lys Ala Val Ser Asp Tyr Phe Gly Gly Ser Cys Val Pro Gly Ala
165 170 175

Gly Glu Thr Ser Tyr Ser Glu Ser Leu Cys Arg Leu Cys Arg Gly Asp
180 185 190

Ser Ser Gly Glu Gly Val Cys Asp Lys Ser Pro Leu Glu Arg Tyr Tyr
195 200 205

Asp Tyr Ser Gly Ala Phe Arg Cys Leu Ala Glu Gly Ala Gly Asp Val
210 215 220

Ala Phe Val Lys His Ser Thr Val Leu Glu Asn Thr Asp Gly Lys Thr
225 230 235 240

Leu Pro Ser Trp Gly Gln Ala Leu Leu Ser Gln Asp Phe Glu Leu Leu
245 250 255

Cys Arg Asp Gly Ser Arg Ala Asp Val Thr Glu Trp Arg Gln Cys His
260 265 270

Leu Ala Arg Val Pro Ala His Ala Val Val Val Arg Ala Asp Thr Asp

275

280

285

Gly Gly Leu Ile Phe Arg Leu Leu Asn Glu Gly Gln Arg Leu Phe Ser
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His Glu Gly Ser Ser Phe Gln Met Phe Ser Ser Glu Ala Tyr Gly Gln
305 310 315 320

Lys Asp Leu Leu Phe Lys Asp Ser Thr Ser Glu Leu Val Pro Ile Ala
325 330 335

Thr Gln Thr Tyr Glu Ala Trp Leu Gly His Glu Tyr Leu His Ala Met
340 345 350

Lys Gly Leu Leu Cys Asp Pro Asn Arg Leu Pro Pro Tyr Leu Arg Trp
355 360 365

Cys Val Leu Ser Thr Pro Glu Ile Gln Lys Cys Gly Asp Met Ala Val
370 375 380

Ala Phe Arg Arg Gln Arg Leu Lys Pro Glu Ile Gln Cys Val Ser Ala
385 390 395 400

Lys Ser Pro Gln His Cys Met Glu Arg Ile Gln Ala Glu Gln Val Asp
405 410 415

Ala Val Thr Leu Ser Gly Glu Asp Ile Tyr Thr Ala Gly Lys Lys Tyr
420 425 430

Gly Leu Val Pro Ala Ala Gly Glu His Tyr Ala Pro Glu Asp Ser Ser
435 440 445

Asn Ser Tyr Tyr Val Val Ala Val Val Arg Arg Asp Ser Ser His Ala
450 455 460

Phe Thr Leu Asp Glu Leu Arg Gly Lys Arg Ser Cys His Ala Gly Phe
465 470 475 480

Gly Ser Pro Ala Gly Trp Asp Val Pro Val Gly Ala Leu Ile Gln Arg
485 490 495

Gly Phe Ile Arg Pro Lys Asp Cys Asp Val Leu Thr Ala Val Ser Glu
500 505 510

Phe Phe Asn Ala Ser Cys Val Pro Val Asn Asn Pro Lys Asn Tyr Pro
515 520 525

Ser Ser Leu Cys Ala Leu Cys Val Gly Asp Glu Gln Gly Arg Asn Lys
530 535 540

Cys Val Gly Asn Ser Gln Glu Arg Tyr Tyr Gly Arg Gly Ala Phe
545 550 555 560

Arg Cys Leu Val Glu Asn Ala Gly Asp Val Ala Phe Val Arg His Thr
565 570 575

Thr Val Phe Asp Asn Thr Asn Gly His Asn Ser Glu Pro Trp Ala Ala
580 585 590

Glu Leu Arg Ser Glu Asp Tyr Glu Leu Leu Cys Pro Asn Gly Ala Arg
595 600 605

Ala Glu Val Ser Gln Phe Ala Ala Cys Asn Leu Ala Gln Ile Pro Pro
610 615 620

His Ala Val Met Val Arg Pro Asp Thr Asn Ile Phe Thr Val Tyr Gly
625 630 635 640

Leu Leu Asp Lys Ala Gln Asp Leu Phe Gly Asp Asp His Asn Lys Asn
645 650 655

Gly Phe Lys Met Phe Asp Ser Ser Asn Tyr His Gly Gln Asp Leu Leu
660 665 670

Phe Lys Asp Ala Thr Val Arg Ala Val Pro Val Gly Glu Lys Thr Thr
675 680 685

Tyr Arg Gly Trp Leu Gly Leu Asp Tyr Val Ala Ala Leu Glu Gly Met
690 695 700

Ser Ser Gln Gln Cys Ser Gly Ala Ala Ala Pro Ala Pro Gly Ala Pro
705 710 715 720

Leu Leu Pro Leu Leu Leu Pro Ala Leu Ala Ala Arg Leu Leu Pro Pro
725 730 735

Ala Leu